SEQUENCE LISTING

<110> Yunn-Bor Yang
      Chia-Li Wei
      Jyh-Shing Hsu
      Ying-Chieh Tsai

<120> Mutated Penicillin Expandase and Process for Preparing 7-ADCA Using
      the Same

<130> 6653-017-999

<140> To Be Assigned
<141> 2002-03-26

<160> 1

<170> FastSEQ for Windows Version 4.0

<210> 1
<211> 1230
<212> DNA
<213> Streptomyces clavuligerus

<220>
<221> CDS
<222> (232)...(1164)

<400> 1
cccgggtgcc gctggtcagc gccaccggat cgacccgtat gggccgcgcc gtgggccccc   60
gggccggtgc tccggatctc ggcgaacttc tacaccaccg aagaggagat cgaccgcctg   120
gcggacgcgc tggacgcgct gacgggcgag tgatccccccc ggctcgcgga ccgcctcccc   180
cgcgctgttg accacccggt tcacggatta cgagaggatc agtgagagtt g atg gac   237
                                                        Met Asp
                                                          1

acg acg gtg ccc acc ttc agc ctg gcc gaa ctc cag cag ggc ctg cac   285
Thr Thr Val Pro Thr Phe Ser Leu Ala Glu Leu Gln Gln Gly Leu His
          5   10   15

cag gac gag ttc cgc agg tgt ctg agg gac aag ggc ctc ttc tat ctg   333
Gln Asp Glu Phe Arg Arg Cys Leu Arg Asp Lys Gly Leu Phe Tyr Leu
    20   25   30

acg gac tgc ggt ctg acc gac acc gag ctg aag tcg gcc aag gac atc   381
Thr Asp Cys Gly Leu Thr Asp Thr Glu Leu Lys Ser Ala Lys Asp Ile
35   40   45   50

gtc atc gac ttc ttc gag cac ggc agc gag gcg gag aag cgc gcc gtc   429
Val Ile Asp Phe Phe Glu His Gly Ser Glu Ala Glu Lys Arg Ala Val
                    55   60   65

acc tcg ccc gtc ccc acc atg cgc cgc ggc ttc acc ggg ctg gag tcg   477
Thr Ser Pro Val Pro Thr Met Arg Arg Gly Phe Thr Gly Leu Glu Ser
                70   75   80

gag agc acc gcc cag atc acc aat acc ggc agc tac tcc gac tac tcg   525
Glu Ser Thr Ala Gln Ile Thr Asn Thr Gly Ser Tyr Ser Asp Tyr Ser
            85   90   95

-1-

```
atg tgc tac tcg atg ggc acc gcg gac aac ctc ttc ccg tcc ggt gac       573
Met Cys Tyr Ser Met Gly Thr Ala Asp Asn Leu Phe Pro Ser Gly Asp
    100             105             110

ttc gag cgg atc tgg acc cag tac ttc gac cgc cag tac acc gcc tcc       621
Phe Glu Arg Ile Trp Thr Gln Tyr Phe Asp Arg Gln Tyr Thr Ala Ser
115             120             125             130

cgc gcg gtc gcc cgg gag gtc ctg cgg gcg acc ggg acc gag ccc gac       669
Arg Ala Val Ala Arg Glu Val Leu Arg Ala Thr Gly Thr Glu Pro Asp
                135             140             145

ggc ggg gtc gag gcc ttc ctc gac tgc gag ccg ctg ctg cgg ttc cgc       717
Gly Gly Val Glu Ala Phe Leu Asp Cys Glu Pro Leu Leu Arg Phe Arg
            150             155             160

tac ttc ccg cag gtc ccc gag cac cgc agc gcc gag gag cag ccc ctg       765
Tyr Phe Pro Gln Val Pro Glu His Arg Ser Ala Glu Glu Gln Pro Leu
        165             170             175

cgg atg gcg ccg cac tac gac ctg tcg atg gtc acc ctc atc cag cag       813
Arg Met Ala Pro His Tyr Asp Leu Ser Met Val Thr Leu Ile Gln Gln
        180             185             190

aca ccc tgc gcc aac ggc ttc gtc agc ctc cag gcc gag gtc ggc ggc       861
Thr Pro Cys Ala Asn Gly Phe Val Ser Leu Gln Ala Glu Val Gly Gly
195             200             205             210

gcg ttc acg gac ctg ccc tac cgt ccg gac gcc gtc ctc gtc ttc tgc       909
Ala Phe Thr Asp Leu Pro Tyr Arg Pro Asp Ala Val Leu Val Phe Cys
                215             220             225

ggc gcc atc gcg acc ctg gtg acc ggc ggc cag gtc aag gcc ccc cgg       957
Gly Ala Ile Ala Thr Leu Val Thr Gly Gly Gln Val Lys Ala Pro Arg
            230             235             240

cac cat gtc gcg gcc ccc cgc agg gac cag ata gcg ggc agc agc cgc      1005
His His Val Ala Ala Pro Arg Arg Asp Gln Ile Ala Gly Ser Ser Arg
        245             250             255

acc tcc agt gtg ttc ttc ctc cgt ccc aac gcg gac ttc acc ttc tcc      1053
Thr Ser Ser Val Phe Phe Leu Arg Pro Asn Ala Asp Phe Thr Phe Ser
260             265             270

gtc ccg ctg gcg cgc gag tgc ggc ttc gat gtc agc ctg gac ggc gag      1101
Val Pro Leu Ala Arg Glu Cys Gly Phe Asp Val Ser Leu Asp Gly Glu
275             280             285             290

acc gcc acg ttc cag gat tgg atc ggg ggc aac tac gtg aac atc cgc      1149
Thr Ala Thr Phe Gln Asp Trp Ile Gly Gly Asn Tyr Val Asn Ile Arg
            295             300             305

cgc aca tcc aag gca tagagagcac acaccgtcat ggtcacagca gcaatcagtg      1204
Arg Thr Ser Lys Ala
            310

gtaccgacga gatacgcgcg agggcg                                         1230
```